Supporting Material

PDB ID	Residue A	Atom A	Residue B	Atom B	Distance (Å)
COMPLEX	E_LYS_34	NZ	E_ASP_38	OD2	3.406
COMPLEX	E_ARG_76	NH2	E_GLU_80	OE2	3.282
COMPLEX	E_LYS_88	NZ	E_ASP_85	OD1	3.561
COMPLEX	E_ARG_93	NH1	E_ASP_496	OD2	3.690
COMPLEX	E_ARG_93	NH2	E_ASP_496	OD2	3.173
COMPLEX	E_LYS_106	NZ	E_GLU_103	OE2	2.937
COMPLEX	E_LYS_128	NZ	E_ASP_234	OD1	2.943
COMPLEX	E_LYS_128	NZ	E_ASP_234	OD2	3.046
COMPLEX	E_ARG_135	NH1	E_ASP_130	OD2	3.486
COMPLEX	E_ARG_135	NH2	E_ASP_130	OD2	3.070
COMPLEX	E_ARG_144	NH2	E_ASP_129	OD2	3.183
COMPLEX	E_HIS_167	NE2	E_ASP_234	OD2	2.828
COMPLEX	E_ARG_195	NH1	E_GLU_191	OE2	3.248
COMPLEX	E_ARG_197	NH1	E_ASP_152	OD2	3.449
COMPLEX	E_ARG_216	NH2	E_ASP_190	OD1	2.962
COMPLEX	E_ARG_216	NH2	E_ASP_190	OD2	2.998
COMPLEX	E_ARG_228	NH1	E_GLU_137	OE2	2.973
COMPLEX	E_LYS_232	NZ	E_ASP_225	OD2	2.917
COMPLEX	E_ARG_240	NH1	E_GLU_278	OE1	2.961
COMPLEX	E_ARG_240	NH2	E_GLU_278	OE1	2.876
COMPLEX	E_ARG_240	NH2	E_GLU_278	OE2	3.881
COMPLEX	E_ARG_240	NH2	E_GLU_281	OE1	3.033
COMPLEX	E_LYS_252	NZ	E_ASP_287	OD1	2.978
COMPLEX	E_LYS_252	NZ	E_ASP_287	OD2	3.195
COMPLEX	E_LYS_316	NZ	E_ASP_320	OD2	3.051
COMPLEX	E_LYS_319	NZ	E_GLU_281	OE2	2.856
COMPLEX	E_LYS_334	NZ	E_GLU_371	OE1	2.936
COMPLEX	E_ARG_351	NH2	E_ASP_253	OD2	2.981
COMPLEX	E_LYS_381	NZ	E_ASP_379	OD2	2.905
COMPLEX	E_ARG_383	NH1	E_GLU_1054	OE1	2.853
COMPLEX	E_ARG_383	NH1	E_GLU_1054	OE2	3.495
COMPLEX	E_ARG_383	NH2	E_GLU_1054	OE1	3.460
COMPLEX	E_ARG_383	NH2	E_GLU_1054	OE2	2.828
COMPLEX	E_ARG_396	NH1	E_GLU_412	OE2	2.893
COMPLEX	E_ARG_420	NH1	E_ASP_171	OD2	3.640
COMPLEX	E_ARG_432	NH1	E_GLU_1054	OE1	3.040
COMPLEX	E_LYS_442	NZ	E_GLU_105	OE1	2.864
COMPLEX	E_LYS_442	NZ	E_GLU_105	OE2	3.135
COMPLEX	E_LYS_442	NZ	E_ASP_439	OD1	3.264
COMPLEX	E_LYS_476	NZ	E_GLU_474	OE1	3.939
COMPLEX	E_ARG_499	NH1	E_ASP_496	OD1	3.784
COMPLEX	E_ARG_503	NH1	E_GLU_748	OE2	3.059
COMPLEX	E_ARG_503	NH2	E_GLU_748	OE2	2.869
COMPLEX	E_HIS_524	NE2	E_GLU_546	OE2	2.888
COMPLEX	E_LYS_552	NZ	E_GLU_546	OE1	2.881
COMPLEX	E_ARG_556	NH2	E_ASP_541	OD1	2.849
COMPLEX	E_ARG_556	NH2	E_ASP_541	OD2	3.687
COMPLEX	E_LYS_558	NZ	E_GLU_563	OE1	3.095
COMPLEX	E_LYS_567	NZ	E_GLU_554	OE1	2.965
COMPLEX	E_LYS_567	NZ	E_GLU_554	OE2	3.258
COMPLEX	E_ARG_579	NH2	E_ASP_577	OD2	3.280
COMPLEX	E_ARG_586	NH1	E_ASP_757	OD1	2.992
COMPLEX	E_ARG_586	NH1	E_ASP_757	OD2	3.188
COMPLEX	E_ARG_586	NH2	E_ASP_757	OD1	2.880
COMPLEX	E_LYS_615	NZ	E_ASP_66	OD1	2.903
COMPLEX	E_LYS_626	NZ	E_GLU_618	OE1	2.874
COMPLEX	E_LYS_627	NZ	E_GLU_634	OE2	2.912

COMPLEX	E_LYS_629	NZ	E_ASP_632	OD1	3.949
COMPLEX	E_LYS_631	NZ	E_GLU_643	OE2	2.891
COMPLEX	E_ARG_677	NH1	E_GLU_673	OE1	3.745
COMPLEX	E_ARG_677	NH1	E_GLU_673	OE2	3.823
COMPLEX	E_ARG_677	NH2	E_GLU_673	OE1	3.292
COMPLEX	E_ARG_692	NH1	E_ASP_696	OD1	3.071
COMPLEX	E_ARG_754	NH1	E_ASP_843	OD1	2.918
COMPLEX	E_ARG_754	NH2	E_ASP_582	OD1	2.830
COMPLEX	E_ARG_754	NH2	E_ASP_582	OD2	3.691
COMPLEX	E_ARG_754	NH2	E_ASP_843	OD1	3.006
COMPLEX	E_ARG_754	NH2	E_ASP_843	OD2	2.886
COMPLEX	E_LYS_815	NZ	E_GLU_811	OE1	3.704
COMPLEX	E_ARG_819	NH1	E_GLU_42	OE1	3.010
COMPLEX	E_ARG_831	NH1	E_ASP_853	OD1	3.160
COMPLEX	E_ARG_831	NH1	E_ASP_853	OD2	3.071
COMPLEX	E_HIS_852	ND1	E_ASP_837	OD1	2.865
COMPLEX	E_HIS_852	ND1	E_ASP_837	OD2	3.063
COMPLEX	E_HIS_852	NE2	E_ASP_834	OD1	3.522
COMPLEX	E_ARG_861	NH2	E_GLU_865	OE1	3.579
COMPLEX	E_LYS_976	NZ	E_ASP_38	OD1	3.624
COMPLEX	E_ARG_989	NH1	E_ASP_867	OD2	3.373
COMPLEX	E_ARG_989	NH2	E_ASP_867	OD1	3.813
COMPLEX	E_ARG_989	NH2	E_ASP_867	OD2	2.899
COMPLEX	E_LYS_1036	NZ	E_ASP_1033	OD1	3.076
COMPLEX	E_ARG_1039	NH1	E_ASP_541	OD1	3.692
COMPLEX	E_ARG_1039	NH1	E_ASP_544	OD1	3.478
COMPLEX	E_ARG_1039	NH1	E_ASP_544	OD2	3.638
COMPLEX	E_ARG_1039	NH2	E_ASP_544	OD1	2.956
COMPLEX	E_LYS_1042	NZ	E_ASP_561	OD1	3.153

Table 1: Salt bridging networks within the structural model represented in COMPLEX.pdb. In this table, the residue naming scheme is **Chain ID_residue name_residue number**.

Count	Residue A	Residue B
4	ARG383	GLU1054
3	ARG1039	ASP544
3	ARG754	ASP843
3	ARG677	GLU673
3	ARG240	GLU278
3	ARG586	ASP757
3	ARG989	ASP867
2	LYS128	ASP234
2	ARG93	ASP496
2	ARG831	ASP853
2	HIS852	ASP837
2	ARG754	ASP582
2	LYS252	ASP287
2	ARG503	GLU748
2	LYS567	GLU554
2	ARG135	ASP130
2	LYS442	GLU105
2	ARG556	ASP541
2	ARG216	ASP190
1	ARG396	GLU412
1	LYS334	GLU371
1	LYS976	ASP38
1	LYS319	GLU281
1	ARG228	GLU137
1	LYS1036	ASP1033
1	LYS381	ASP379
1	LYS88	ASP85
1	LYS558	GLU563
1	LYS626	GLU618
1	LYS627	GLU634
1	ARG197	ASP152
1	ARG432	GLU1054
1	LYS629	ASP632
1	ARG819	GLU42
1	LYS442	ASP439
1	LYS1042	ASP561
1	LYS316	ASP320
1	LYS476	GLU474
1	ARG195	GLU191
1	LYS552	GLU546
1	LYS631	GLU643
1	ARG499	ASP496
1	ARG1039	ASP541
1	ARG861	GLU865
1	ARG351	ASP253
1	HIS852	ASP834
1	ARG579	ASP577
1	ARG144	ASP129
1	LYS615	ASP66
1	ARG76	GLU80
1	ARG420	ASP171
1	LYS232	ASP225
1	ARG692	ASP696
1	LYS106	GLU103
1	LYS815	GLU811
1	LYS34	ASP38
1	HIS167	ASP234

1	HIS524	GLU546
1	ARG240	GLU281

Table 2: Counting of side chain salt bridging networks within the structural model represented in COMPLEX.pdb. In this table, the residue naming scheme is **Chain ID_residue name_residue number**.

PDB	Acceptor (A)	Donor (D)	Hydrogen (H)	D-A (Å)	H-A (Å)	$\angle ADH$(°)
COMPLEX.PDB	OG, E_SER_29	OG1, E_THR_32	HG1, E_THR_32	2.72	1.76	6.24
COMPLEX.PDB	O, E_SER_29	N, E_ILE_33	H, E_ILE_33	2.98	1.99	11.71
COMPLEX.PDB	O, E_PRO_30	N, E_LYS_34	H, E_LYS_34	2.87	1.92	16.05
COMPLEX.PDB	O, E_VAL_31	N, E_SER_35	H, E_SER_35	2.95	1.95	8.95
COMPLEX.PDB	O, E_THR_32	N, E_TRP_36	H, E_TRP_36	2.94	2.02	20.41
COMPLEX.PDB	O, E_ILE_33	N, E_VAL_37	H, E_VAL_37	2.83	1.84	9.15
COMPLEX.PDB	O, E_LYS_34	N, E_ASP_38	H, E_ASP_38	2.90	1.94	15.40
COMPLEX.PDB	O, E_VAL_37	N, E_GLN_41	H, E_GLN_41	2.82	1.84	12.90
COMPLEX.PDB	O, E_MET_997	NE2, E_GLN_41	2HE2, E_GLN_41	2.88	1.96	20.18
COMPLEX.PDB	O, E_ASP_38	N, E_GLU_42	H, E_GLU_42	2.90	1.90	6.43
COMPLEX.PDB	O, E_GLN_41	N, E_VAL_45	H, E_VAL_45	2.93	1.93	6.80
COMPLEX.PDB	O, E_GLU_42	N, E_THR_46	H, E_THR_46	2.92	1.94	12.04
COMPLEX.PDB	O, E_GLU_42	OG1, E_THR_46	HG1, E_THR_46	2.70	1.75	11.54
COMPLEX.PDB	O, E_LEU_44	N, E_ALA_48	H, E_ALA_48	2.91	1.92	10.10
COMPLEX.PDB	O, E_VAL_45	N, E_LYS_49	H, E_LYS_49	2.91	1.91	10.32
COMPLEX.PDB	O, E_THR_46	N, E_THR_50	H, E_THR_50	2.90	1.90	7.94
COMPLEX.PDB	O, E_ALA_48	OG, E_SER_52	HG, E_SER_52	2.67	1.70	3.58
COMPLEX.PDB	O, E_GLY_53	N, E_LEU_57	H, E_LEU_57	2.99	2.00	11.30
COMPLEX.PDB	O, E_THR_55	N, E_ASP_59	H, E_ASP_59	2.81	1.86	15.65
COMPLEX.PDB	O, E_ALA_58	N, E_GLU_62	H, E_GLU_62	2.97	1.95	3.78
COMPLEX.PDB	O, E_ASP_59	N, E_LYS_63	H, E_LYS_63	2.81	1.98	28.81
COMPLEX.PDB	OE1, E_GLU_702	OH, E_TYR_64	HH, E_TYR_64	2.63	1.66	4.27
COMPLEX.PDB	O, E_GLU_62	NE2, E_GLN_65	2HE2, E_GLN_65	2.89	1.89	7.15
COMPLEX.PDB	O, E_TYR_61	OH, E_TYR_68	HH, E_TYR_68	2.64	1.68	4.45
COMPLEX.PDB	O, E_LYS_613	N, E_THR_69	H, E_THR_69	2.87	1.87	10.16
COMPLEX.PDB	O, E_TYR_611	N, E_GLU_71	H, E_GLU_71	2.94	1.94	8.57
COMPLEX.PDB	O, E_PHE_609	N, E_ASN_73	H, E_ASN_73	2.80	1.80	9.55
COMPLEX.PDB	O, E_THR_505	ND2, E_ASN_73	1HD2, E_ASN_73	2.99	1.98	2.88
COMPLEX.PDB	O, E_SER_608	ND2, E_ASN_73	2HD2, E_ASN_73	2.95	1.96	7.57
COMPLEX.PDB	O, E_ASN_74	N, E_LEU_78	H, E_LEU_78	2.90	1.92	11.61
COMPLEX.PDB	O, E_ALA_75	N, E_VAL_79	H, E_VAL_79	2.90	1.90	9.25
COMPLEX.PDB	O, E_GLN_77	N, E_ILE_81	H, E_ILE_81	2.99	2.00	10.15
COMPLEX.PDB	O, E_VAL_79	N, E_ALA_83	H, E_ALA_83	2.81	1.84	13.88
COMPLEX.PDB	O, E_ILE_81	N, E_ASP_85	H, E_ASP_85	2.89	1.93	15.53
COMPLEX.PDB	O, E_ALA_82	N, E_ILE_86	H, E_ILE_86	2.93	1.94	11.58
COMPLEX.PDB	O, E_ALA_83	N, E_GLU_87	H, E_GLU_87	2.87	1.91	15.42
COMPLEX.PDB	O, E_ARG_84	N, E_LYS_88	H, E_LYS_88	2.93	1.97	15.42
COMPLEX.PDB	O, E_ASP_85	N, E_LEU_89	H, E_LEU_89	2.96	2.02	17.81
COMPLEX.PDB	O, E_GLU_87	N, E_SER_91	H, E_SER_91	2.84	1.86	13.38
COMPLEX.PDB	O, E_ASP_491	NH2, E_ARG_93	1HH2, E_ARG_93	2.89	1.92	15.11
COMPLEX.PDB	O, E_LEU_90	N, E_SER_94	H, E_SER_94	2.84	1.88	15.66
COMPLEX.PDB	O, E_LEU_90	OG, E_SER_94	HG, E_SER_94	2.86	1.90	5.63
COMPLEX.PDB	O, E_SER_91	N, E_LYS_95	H, E_LYS_95	2.89	1.97	20.98
COMPLEX.PDB	O, E_LEU_97	N, E_ALA_101	H, E_ALA_101	2.89	1.90	11.14
COMPLEX.PDB	O, E_ARG_99	N, E_GLU_103	H, E_GLU_103	2.96	1.99	14.24
COMPLEX.PDB	O, E_LEU_100	N, E_ALA_104	H, E_ALA_104	2.91	1.94	14.04
COMPLEX.PDB	OE2, E_GLU_103	NZ, E_LYS_106	1HZ, E_LYS_106	2.94	1.96	12.59
COMPLEX.PDB	O, E_GLU_103	N, E_VAL_107	H, E_VAL_107	2.87	1.88	11.34
COMPLEX.PDB	O, E_ALA_104	N, E_GLN_108	H, E_GLN_108	2.95	1.96	9.59
COMPLEX.PDB	O, E_GLU_105	N, E_ALA_109	H, E_ALA_109	2.96	2.01	16.14
COMPLEX.PDB	O, E_GLN_108	N, E_HIS_111	H, E_HIS_111	3.00	2.03	14.52
COMPLEX.PDB	OD1, E_ASN_184	NE2, E_HIS_111	HE2, E_HIS_111	2.88	1.88	10.04
COMPLEX.PDB	OE2, E_GLU_115	NE1, E_TRP_113	HE1, E_TRP_113	2.99	2.09	21.85
COMPLEX.PDB	OD2, E_ASP_116	OG, E_SER_119	HG, E_SER_119	2.66	1.71	9.60
COMPLEX.PDB	O, E_PHE_117	N, E_ASN_120	H, E_ASN_120	2.99	2.06	18.33
COMPLEX.PDB	O, E_GLY_141	N, E_VAL_122	H, E_VAL_122	2.90	1.88	3.47
COMPLEX.PDB	O, E_GLN_143	N, E_TYR_124	H, E_TYR_124	2.94	1.94	9.51

COMPLEX.PDB	O, E_VAL_166	N, E_ALA_127	H, E_ALA_127	2.82	1.81	5.33
COMPLEX.PDB	O, E_ILE_168	NZ, E_LYS_128	2HZ, E_LYS_128	2.87	1.98	22.93
COMPLEX.PDB	OD1, E_ASP_234	NZ, E_LYS_128	3HZ, E_LYS_128	2.94	1.95	10.09
COMPLEX.PDB	OD1, E_ASP_132	N, E_GLU_134	H, E_GLU_134	2.99	2.01	12.34
COMPLEX.PDB	O, E_VAL_122	N, E_GLN_143	H, E_GLN_143	2.90	1.95	16.43
COMPLEX.PDB	OD2, E_ASP_129	NE, E_ARG_144	HE, E_ARG_144	2.79	1.81	12.37
COMPLEX.PDB	O, E_TYR_124	N, E_ILE_145	H, E_ILE_145	2.87	1.87	9.22
COMPLEX.PDB	O, E_ALA_153	N, E_PHE_155	H, E_PHE_155	2.88	1.97	21.04
COMPLEX.PDB	O, E_PRO_222	NH2, E_ARG_157	1HH2, E_ARG_157	2.99	2.09	21.27
COMPLEX.PDB	O, E_ILE_150	N, E_ILE_159	H, E_ILE_159	2.80	1.81	10.78
COMPLEX.PDB	O, E_ALA_220	N, E_SER_160	H, E_SER_160	2.81	1.87	17.92
COMPLEX.PDB	O, E_ALA_164	ND1, E_HIS_163	HD1, E_HIS_163	2.95	1.96	10.60
COMPLEX.PDB	OD2, E_ASP_190	N, E_ALA_164	H, E_ALA_164	2.89	1.87	1.22
COMPLEX.PDB	O, E_TYR_217	N, E_ALA_165	H, E_ALA_165	2.83	1.83	8.61
COMPLEX.PDB	O, E_TYR_125	N, E_VAL_166	H, E_VAL_166	2.85	1.84	4.85
COMPLEX.PDB	O, E_ALA_215	N, E_HIS_167	H, E_HIS_167	2.88	1.88	9.81
COMPLEX.PDB	OD2, E_ASP_234	NE2, E_HIS_167	HE2, E_HIS_167	2.83	1.86	15.02
COMPLEX.PDB	O, E_SER_176	N, E_LEU_180	H, E_LEU_180	2.87	1.87	6.50
COMPLEX.PDB	O, E_THR_177	N, E_ASN_181	H, E_ASN_181	2.90	1.93	13.02
COMPLEX.PDB	O, E_ARG_114	ND2, E_ASN_181	1HD2, E_ASN_181	2.93	1.99	18.40
COMPLEX.PDB	O, E_VAL_179	N, E_LEU_183	H, E_LEU_183	2.86	1.86	6.86
COMPLEX.PDB	O, E_LEU_180	N, E_ASN_184	H, E_ASN_184	2.93	1.99	18.73
COMPLEX.PDB	OE2, E_GLU_182	NE1, E_TRP_185	HE1, E_TRP_185	2.92	1.92	8.41
COMPLEX.PDB	O, E_GLU_182	N, E_THR_186	H, E_THR_186	2.89	1.89	8.76
COMPLEX.PDB	O, E_GLU_182	OG1, E_THR_186	HG1, E_THR_186	2.66	1.70	3.98
COMPLEX.PDB	O, E_LEU_189	N, E_PHE_193	H, E_PHE_193	2.87	1.89	12.18
COMPLEX.PDB	O, E_GLU_191	N, E_ARG_195	H, E_ARG_195	2.96	1.97	11.10
COMPLEX.PDB	OE1, E_GLN_206	ND2, E_ASN_196	2HD2, E_ASN_196	2.92	1.94	11.76
COMPLEX.PDB	O, E_LYS_194	N, E_ASP_198	H, E_ASP_198	2.81	1.86	16.26
COMPLEX.PDB	OD1, E_ASP_200	N, E_THR_202	H, E_THR_202	2.95	2.00	17.00
COMPLEX.PDB	OD1, E_ASP_200	OG1, E_THR_202	HG1, E_THR_202	2.72	1.76	6.38
COMPLEX.PDB	O, E_TYR_218	N, E_GLN_206	H, E_GLN_206	2.96	2.07	23.24
COMPLEX.PDB	O, E_PHE_193	NE2, E_GLN_206	1HE2, E_GLN_206	2.97	1.99	10.64
COMPLEX.PDB	O, E_GLY_489	N, E_VAL_207	H, E_VAL_207	2.81	1.87	18.28
COMPLEX.PDB	O, E_ARG_216	N, E_PHE_208	H, E_PHE_208	2.90	1.91	10.14
COMPLEX.PDB	O, E_VAL_487	N, E_GLY_209	H, E_GLY_209	2.86	1.85	8.10
COMPLEX.PDB	O, E_LEU_214	N, E_SER_210	H, E_SER_210	2.78	1.80	12.47
COMPLEX.PDB	OE1, E_GLU_182	OG, E_SER_210	HG, E_SER_210	2.66	1.69	4.87
COMPLEX.PDB	O, E_LEU_485	N, E_ALA_211	H, E_ALA_211	2.82	1.81	5.49
COMPLEX.PDB	O, E_SER_210	N, E_GLY_213	H, E_GLY_213	2.97	1.99	12.83
COMPLEX.PDB	O, E_HIS_167	N, E_ALA_215	H, E_ALA_215	2.93	1.94	10.87
COMPLEX.PDB	O, E_PHE_208	N, E_ARG_216	H, E_ARG_216	2.86	1.87	11.52
COMPLEX.PDB	OD1, E_ASP_190	NE, E_ARG_216	HE, E_ARG_216	2.91	2.02	23.66
COMPLEX.PDB	OD2, E_ASP_190	NH2, E_ARG_216	1HH2, E_ARG_216	3.00	2.07	19.79
COMPLEX.PDB	O, E_ALA_165	N, E_TYR_217	H, E_TYR_217	2.87	1.89	12.53
COMPLEX.PDB	O, E_GLN_206	N, E_TYR_218	H, E_TYR_218	2.80	1.82	12.63
COMPLEX.PDB	O, E_TYR_161	OH, E_TYR_218	HH, E_TYR_218	2.74	1.78	6.58
COMPLEX.PDB	O, E_SER_160	N, E_ALA_220	H, E_ALA_220	2.95	2.06	23.78
COMPLEX.PDB	O, E_PRO_222	OG, E_SER_221	HG, E_SER_221	2.90	1.93	1.12
COMPLEX.PDB	OD1, E_ASP_130	OG1, E_THR_229	HG1, E_THR_229	2.76	1.81	9.95
COMPLEX.PDB	OD2, E_ASP_225	NZ, E_LYS_232	2HZ, E_LYS_232	2.92	1.96	15.31
COMPLEX.PDB	OD1, E_ASP_237	N, E_ARG_239	H, E_ARG_239	2.92	1.95	14.36
COMPLEX.PDB	O, E_ALA_211	NH1, E_ARG_239	1HH1, E_ARG_239	2.92	1.92	7.26
COMPLEX.PDB	OE1, E_GLU_278	NH1, E_ARG_240	2HH1, E_ARG_240	2.96	2.06	22.46
COMPLEX.PDB	OE1, E_GLU_278	NH2, E_ARG_240	2HH2, E_ARG_240	2.88	1.94	17.95
COMPLEX.PDB	O, E_VAL_238	N, E_ARG_241	H, E_ARG_241	2.97	2.00	13.82
COMPLEX.PDB	O, E_PRO_242	N, E_GLN_246	H, E_GLN_246	2.91	1.95	15.17
COMPLEX.PDB	OE1, E_GLN_445	NE2, E_GLN_246	2HE2, E_GLN_246	2.93	1.98	15.85

COMPLEX.PDB	O, E_TYR_244	N, E_ALA_248	H, E_ALA_248	2.82	1.94	24.44
COMPLEX.PDB	OD1, E_ASP_287	N, E_LYS_252	H, E_LYS_252	2.89	1.95	18.35
COMPLEX.PDB	OD1, E_ASP_287	NZ, E_LYS_252	3HZ, E_LYS_252	2.98	1.98	8.55
COMPLEX.PDB	O, E_ASN_355	N, E_ASP_253	H, E_ASP_253	2.84	1.82	3.42
COMPLEX.PDB	O, E_PHE_288	N, E_MET_254	H, E_MET_254	2.83	1.83	8.82
COMPLEX.PDB	O, E_MET_359	N, E_LEU_257	H, E_LEU_257	2.81	1.83	12.48
COMPLEX.PDB	OD1, E_ASP_259	N, E_SER_261	H, E_SER_261	2.96	2.00	16.17
COMPLEX.PDB	OD1, E_ASP_259	OG, E_SER_261	HG, E_SER_261	2.70	1.76	11.26
COMPLEX.PDB	O, E_GLY_329	N, E_GLY_262	H, E_GLY_262	2.86	1.86	7.33
COMPLEX.PDB	OD2, E_ASP_363	OG, E_SER_263	HG, E_SER_263	2.97	2.07	18.12
COMPLEX.PDB	O, E_GLY_262	OG, E_SER_265	HG, E_SER_265	2.89	1.95	11.90
COMPLEX.PDB	O, E_LEU_267	N, E_LEU_271	H, E_LEU_271	2.96	1.96	8.43
COMPLEX.PDB	O, E_THR_268	N, E_ILE_272	H, E_ILE_272	2.84	1.86	13.90
COMPLEX.PDB	O, E_LEU_271	N, E_SER_275	H, E_SER_275	2.83	1.88	16.12
COMPLEX.PDB	O, E_LEU_271	OG, E_SER_275	HG, E_SER_275	2.76	1.80	5.08
COMPLEX.PDB	O, E_ILE_272	N, E_VAL_276	H, E_VAL_276	2.88	1.90	12.09
COMPLEX.PDB	O, E_ARG_273	OG, E_SER_277	HG, E_SER_277	2.82	1.86	5.63
COMPLEX.PDB	O, E_THR_274	N, E_GLU_278	H, E_GLU_278	2.94	1.97	13.12
COMPLEX.PDB	O, E_VAL_276	N, E_LEU_280	H, E_LEU_280	2.97	2.01	15.56
COMPLEX.PDB	OE1, E_GLN_424	OG1, E_THR_282	HG1, E_THR_282	2.98	2.03	7.37
COMPLEX.PDB	OD2, E_ASP_287	N, E_SER_284	H, E_SER_284	2.87	1.94	19.09
COMPLEX.PDB	OD2, E_ASP_287	OG, E_SER_284	HG, E_SER_284	2.69	1.72	5.06
COMPLEX.PDB	O, E_LYS_252	N, E_PHE_288	H, E_PHE_288	2.91	1.92	9.47
COMPLEX.PDB	O, E_VAL_308	N, E_VAL_289	H, E_VAL_289	2.82	1.83	10.02
COMPLEX.PDB	OD1, E_ASN_290	N, E_VAL_291	H, E_VAL_291	3.00	2.17	29.08
COMPLEX.PDB	O, E_ILE_256	N, E_ALA_292	H, E_ALA_292	2.94	1.94	10.19
COMPLEX.PDB	O, E_GLN_299	N, E_SER_293	H, E_SER_293	2.82	1.81	3.96
COMPLEX.PDB	O, E_ASN_297	N, E_ASN_295	H, E_ASN_295	2.86	1.84	3.40
COMPLEX.PDB	O, E_LYS_328	ND2, E_ASN_295	2HD2, E_ASN_295	2.88	1.89	9.42
COMPLEX.PDB	O, E_ASN_295	OG, E_SER_296	HG, E_SER_296	2.68	1.77	15.51
COMPLEX.PDB	O, E_SER_293	N, E_GLN_299	H, E_GLN_299	2.89	1.89	7.56
COMPLEX.PDB	O, E_VAL_291	N, E_VAL_301	H, E_VAL_301	2.97	1.97	8.91
COMPLEX.PDB	O, E_LEU_307	ND1, E_HIS_306	HD1, E_HIS_306	2.90	1.95	17.75
COMPLEX.PDB	O, E_VAL_289	N, E_VAL_308	H, E_VAL_308	2.84	1.83	5.19
COMPLEX.PDB	O, E_VAL_308	N, E_ALA_310	H, E_ALA_310	2.76	1.93	28.55
COMPLEX.PDB	OD1, E_ASN_311	N, E_ASN_314	H, E_ASN_314	2.88	1.92	14.82
COMPLEX.PDB	O, E_ASN_311	N, E_LYS_315	H, E_LYS_315	2.94	1.93	7.13
COMPLEX.PDB	O, E_VAL_312	N, E_LYS_316	H, E_LYS_316	2.88	1.95	19.44
COMPLEX.PDB	O, E_LYS_315	N, E_LYS_319	H, E_LYS_319	2.86	1.87	10.80
COMPLEX.PDB	OE2, E_GLU_281	NZ, E_LYS_319	1HZ, E_LYS_319	2.86	2.03	29.01
COMPLEX.PDB	O, E_LYS_316	N, E_ASP_320	H, E_ASP_320	2.86	1.88	11.58
COMPLEX.PDB	O, E_VAL_317	N, E_ALA_321	H, E_ALA_321	2.89	1.90	11.11
COMPLEX.PDB	O, E_LEU_318	N, E_VAL_322	H, E_VAL_322	2.88	1.91	14.12
COMPLEX.PDB	O, E_LYS_319	N, E_ASN_323	H, E_ASN_323	3.00	2.08	20.61
COMPLEX.PDB	O, E_VAL_260	N, E_LYS_328	H, E_LYS_328	2.85	1.91	18.20
COMPLEX.PDB	O, E_GLY_364	OH, E_TYR_333	HH, E_TYR_333	2.75	1.85	17.61
COMPLEX.PDB	OE1, E_GLU_371	NZ, E_LYS_334	3HZ, E_LYS_334	2.94	1.96	13.07
COMPLEX.PDB	OD1, E_ASP_332	N, E_LYS_335	H, E_LYS_335	2.97	1.95	4.47
COMPLEX.PDB	O, E_SER_296	NZ, E_LYS_335	2HZ, E_LYS_335	2.92	1.93	10.18
COMPLEX.PDB	O, E_TYR_333	N, E_PHE_337	H, E_PHE_337	2.86	1.86	8.03
COMPLEX.PDB	O, E_ASN_346	N, E_ASN_348	H, E_ASN_348	2.78	1.91	25.18
COMPLEX.PDB	O, E_LEU_344	NH1, E_ARG_351	2HH1, E_ARG_351	2.80	1.88	20.50
COMPLEX.PDB	OD2, E_ASP_253	NH2, E_ARG_351	1HH2, E_ARG_351	2.98	2.07	20.97
COMPLEX.PDB	OD1, E_ASP_253	N, E_ALA_352	H, E_ALA_352	2.98	1.98	8.84
COMPLEX.PDB	OD2, E_ASP_253	N, E_ASN_353	H, E_ASN_353	2.87	1.92	16.12
COMPLEX.PDB	O, E_PRO_251	N, E_ASN_355	H, E_ASN_355	2.90	1.91	9.74
COMPLEX.PDB	OH, E_TYR_347	NZ, E_LYS_356	1HZ, E_LYS_356	2.92	1.95	13.13
COMPLEX.PDB	O, E_ARG_383	N, E_ILE_358	H, E_ILE_358	2.96	1.98	11.55

COMPLEX.PDB	O, E_LEU_255	N, E_MET_359	H, E_MET_359	2.90	2.03	25.46
COMPLEX.PDB	OH, E_TYR_333	OG1, E_THR_362	HG1, E_THR_362	2.73	1.83	17.19
COMPLEX.PDB	OD1, E_ASP_363	N, E_GLY_364	H, E_GLY_364	2.83	1.93	22.96
COMPLEX.PDB	O, E_ASP_395	N, E_GLY_365	H, E_GLY_365	2.84	1.85	10.07
COMPLEX.PDB	OE2, E_GLU_367	N, E_ALA_369	H, E_ALA_369	2.86	1.94	19.79
COMPLEX.PDB	O, E_GLN_370	N, E_ALA_374	H, E_ALA_374	2.93	2.04	23.80
COMPLEX.PDB	O, E_ILE_372	N, E_TYR_376	H, E_TYR_376	2.90	1.90	8.37
COMPLEX.PDB	O, E_ASN_377	N, E_LYS_380	H, E_LYS_380	2.88	1.96	20.91
COMPLEX.PDB	OD1, E_ASP_379	N, E_LYS_381	H, E_LYS_381	2.97	1.98	11.18
COMPLEX.PDB	O, E_LYS_407	NH1, E_ARG_383	1HH1, E_ARG_383	2.99	2.00	8.92
COMPLEX.PDB	O, E_ILE_358	N, E_PHE_385	H, E_PHE_385	2.97	1.97	8.07
COMPLEX.PDB	O, E_TYR_409	N, E_THR_386	H, E_THR_386	2.97	1.97	10.08
COMPLEX.PDB	O, E_LEU_360	N, E_PHE_387	H, E_PHE_387	2.87	1.96	21.42
COMPLEX.PDB	O, E_TYR_411	N, E_SER_388	H, E_SER_388	2.84	1.84	8.42
COMPLEX.PDB	O, E_ASP_363	OG, E_SER_388	HG, E_SER_388	2.77	1.81	9.13
COMPLEX.PDB	O, E_THR_362	N, E_VAL_389	H, E_VAL_389	2.78	1.76	3.67
COMPLEX.PDB	O, E_ILE_413	N, E_GLY_390	H, E_GLY_390	2.81	1.84	13.35
COMPLEX.PDB	OE2, E_GLU_412	NH1, E_ARG_396	1HH1, E_ARG_396	2.89	1.91	11.57
COMPLEX.PDB	OD1, E_ASP_395	N, E_GLY_397	H, E_GLY_397	2.86	1.93	19.24
COMPLEX.PDB	O, E_ARG_396	N, E_GLN_400	H, E_GLN_400	2.88	1.91	13.05
COMPLEX.PDB	O, E_GLY_397	N, E_TRP_401	H, E_TRP_401	2.89	1.90	11.37
COMPLEX.PDB	O, E_PRO_398	N, E_MET_402	H, E_MET_402	2.95	2.06	23.71
COMPLEX.PDB	O, E_GLN_400	N, E_CYS_404	H, E_CYS_404	2.97	1.97	9.59
COMPLEX.PDB	O, E_TRP_401	N, E_GLU_405	H, E_GLU_405	2.97	1.96	5.62
COMPLEX.PDB	O, E_MET_402	ND2, E_ASN_406	2HD2, E_ASN_406	2.89	1.90	10.58
COMPLEX.PDB	O, E_ALA_403	N, E_GLY_408	H, E_GLY_408	2.87	1.89	13.49
COMPLEX.PDB	OE2, E_GLU_412	OH, E_TYR_410	HH, E_TYR_410	2.72	1.77	11.16
COMPLEX.PDB	O, E_THR_386	N, E_TYR_411	H, E_TYR_411	2.87	1.95	20.28
COMPLEX.PDB	O, E_SER_388	N, E_ILE_413	H, E_ILE_413	2.84	1.84	8.17
COMPLEX.PDB	O, E_ALA_418	ND2, E_ASN_422	2HD2, E_ASN_422	2.88	1.89	7.42
COMPLEX.PDB	O, E_ILE_419	N, E_THR_423	H, E_THR_423	2.95	1.97	12.17
COMPLEX.PDB	O, E_GLY_431	N, E_VAL_435	H, E_VAL_435	2.95	1.95	10.08
COMPLEX.PDB	O, E_VAL_435	N, E_GLY_438	H, E_GLY_438	3.00	2.10	22.79
COMPLEX.PDB	O, E_ASP_439	N, E_LYS_442	H, E_LYS_442	3.00	2.08	20.89
COMPLEX.PDB	O, E_ASN_448	OG1, E_THR_447	HG1, E_THR_447	2.98	2.06	14.27
COMPLEX.PDB	OG1, E_THR_461	OH, E_TYR_450	HH, E_TYR_450	2.76	1.91	23.68
COMPLEX.PDB	OD1, E_ASP_452	N, E_LEU_454	H, E_LEU_454	2.97	2.07	23.06
COMPLEX.PDB	OD2, E_ASP_452	N, E_GLY_457	H, E_GLY_457	2.89	1.89	8.00
COMPLEX.PDB	O, E_TYR_450	N, E_VAL_459	H, E_VAL_459	2.84	1.82	0.96
COMPLEX.PDB	O, E_VAL_492	N, E_ILE_460	H, E_ILE_460	2.97	1.98	12.35
COMPLEX.PDB	OG1, E_THR_447	N, E_THR_461	H, E_THR_461	2.94	1.93	5.82
COMPLEX.PDB	OD1, E_ASP_491	OG1, E_THR_461	HG1, E_THR_461	2.75	1.78	5.29
COMPLEX.PDB	O, E_VAL_490	N, E_GLY_462	H, E_GLY_462	2.86	1.85	6.36
COMPLEX.PDB	O, E_GLN_445	N, E_THR_463	H, E_THR_463	2.83	1.84	10.98
COMPLEX.PDB	O, E_MET_488	N, E_LEU_464	H, E_LEU_464	3.00	2.02	13.26
COMPLEX.PDB	O, E_GLY_486	N, E_VAL_466	H, E_VAL_466	2.85	1.86	11.32
COMPLEX.PDB	OE2, E_GLU_105	N, E_PHE_467	H, E_PHE_467	2.90	1.89	5.51
COMPLEX.PDB	O, E_LYS_480	ND2, E_ASN_468	2HD2, E_ASN_468	2.94	2.03	20.97
COMPLEX.PDB	O, E_VAL_469	OG1, E_THR_470	HG1, E_THR_470	2.84	1.92	14.21
COMPLEX.PDB	O, E_GLY_471	N, E_LYS_476	H, E_LYS_476	2.99	1.98	5.55
COMPLEX.PDB	OD1, E_ASN_475	ND2, E_ASN_478	1HD2, E_ASN_478	2.92	1.93	8.35
COMPLEX.PDB	O, E_ASN_468	ND2, E_ASN_481	2HD2, E_ASN_481	2.98	2.01	12.76
COMPLEX.PDB	O, E_VAL_466	N, E_LEU_485	H, E_LEU_485	2.81	1.85	14.87
COMPLEX.PDB	O, E_GLY_209	N, E_VAL_487	H, E_VAL_487	2.88	1.90	12.57
COMPLEX.PDB	O, E_LEU_464	N, E_MET_488	H, E_MET_488	2.86	1.85	0.65
COMPLEX.PDB	O, E_ILE_460	N, E_VAL_492	H, E_VAL_492	2.92	1.92	9.90
COMPLEX.PDB	OD2, E_ASP_496	N, E_SER_493	H, E_SER_493	2.90	1.93	13.62
COMPLEX.PDB	OD2, E_ASP_496	OG, E_SER_493	HG, E_SER_493	2.79	1.85	10.99

COMPLEX.PDB	O, E_LEU_494	N, E_LYS_498	H, E_LYS_498	2.89	1.93	15.91
COMPLEX.PDB	O, E_ILE_497	N, E_LEU_500	H, E_LEU_500	2.98	2.09	22.88
COMPLEX.PDB	O, E_ILE_497	OG1, E_THR_501	HG1, E_THR_501	2.96	2.04	14.59
COMPLEX.PDB	OE2, E_GLU_748	NH2, E_ARG_503	2HH2, E_ARG_503	2.87	1.91	15.22
COMPLEX.PDB	OH, E_TYR_607	ND2, E_ASN_509	2HD2, E_ASN_509	2.97	2.01	14.80
COMPLEX.PDB	O, E_CYS_507	N, E_GLY_510	H, E_GLY_510	2.89	1.91	11.87
COMPLEX.PDB	OE2, E_GLU_546	OH, E_TYR_511	HH, E_TYR_511	2.64	1.68	7.93
COMPLEX.PDB	O, E_ALA_601	N, E_PHE_513	H, E_PHE_513	2.99	2.00	11.79
COMPLEX.PDB	O, E_LEU_523	N, E_ALA_514	H, E_ALA_514	2.85	1.88	13.32
COMPLEX.PDB	O, E_SER_599	N, E_ILE_515	H, E_ILE_515	2.89	1.90	12.12
COMPLEX.PDB	O, E_TYR_520	N, E_ASP_516	H, E_ASP_516	2.83	1.83	6.83
COMPLEX.PDB	OD1, E_ASP_516	N, E_ASN_518	H, E_ASN_518	2.96	1.95	6.80
COMPLEX.PDB	OD1, E_ASP_286	ND2, E_ASN_518	1HD2, E_ASN_518	2.98	2.02	15.09
COMPLEX.PDB	O, E_ASP_516	N, E_GLY_519	H, E_GLY_519	2.81	1.84	14.07
COMPLEX.PDB	OD1, E_ASP_285	OH, E_TYR_520	HH, E_TYR_520	2.61	1.65	7.75
COMPLEX.PDB	O, E_LEU_540	N, E_VAL_521	H, E_VAL_521	2.89	1.92	12.99
COMPLEX.PDB	O, E_ALA_514	N, E_LEU_522	H, E_LEU_522	2.84	1.93	21.87
COMPLEX.PDB	OE2, E_GLU_546	NE2, E_HIS_524	HE2, E_HIS_524	2.89	1.87	3.11
COMPLEX.PDB	OE1, E_GLN_889	N, E_GLN_528	H, E_GLN_528	2.97	1.96	6.96
COMPLEX.PDB	O, E_VAL_449	N, E_VAL_538	H, E_VAL_538	2.86	1.84	5.35
COMPLEX.PDB	OD2, E_ASP_541	N, E_LEU_543	H, E_LEU_543	2.91	1.90	3.52
COMPLEX.PDB	O, E_ASP_541	N, E_ASP_544	H, E_ASP_544	2.98	2.05	19.81
COMPLEX.PDB	O, E_ASP_541	N, E_ALA_545	H, E_ALA_545	2.88	1.94	17.77
COMPLEX.PDB	OE1, E_GLU_546	NZ, E_LYS_552	1HZ, E_LYS_552	2.88	1.92	14.82
COMPLEX.PDB	O, E_LEU_547	NZ, E_LYS_552	3HZ, E_LYS_552	2.89	1.88	6.83
COMPLEX.PDB	O, E_LYS_552	N, E_ARG_556	H, E_ARG_556	2.91	1.92	12.24
COMPLEX.PDB	OD2, E_ASP_541	NE, E_ARG_556	HE, E_ARG_556	2.92	1.95	14.11
COMPLEX.PDB	OD1, E_ASN_557	NH1, E_ARG_556	1HH1, E_ARG_556	2.90	2.00	22.19
COMPLEX.PDB	OD1, E_ASP_541	NH2, E_ARG_556	1HH2, E_ARG_556	2.85	1.84	6.22
COMPLEX.PDB	O, E_VAL_553	N, E_ASN_557	H, E_ASN_557	2.89	1.90	11.50
COMPLEX.PDB	O, E_GLU_554	N, E_LYS_558	H, E_LYS_558	2.98	2.00	12.10
COMPLEX.PDB	O, E_ARG_556	N, E_ILE_560	H, E_ILE_560	2.89	1.93	14.39
COMPLEX.PDB	O, E_TYR_588	N, E_LYS_567	H, E_LYS_567	2.92	1.94	14.06
COMPLEX.PDB	OE1, E_GLU_554	NZ, E_LYS_567	1HZ, E_LYS_567	2.96	2.06	21.68
COMPLEX.PDB	O, E_ARG_586	N, E_PHE_569	H, E_PHE_569	2.89	1.89	7.99
COMPLEX.PDB	O, E_GLY_584	N, E_THR_571	H, E_THR_571	2.90	1.97	19.39
COMPLEX.PDB	O, E_ASP_582	N, E_VAL_573	H, E_VAL_573	2.78	1.77	2.98
COMPLEX.PDB	OE1, E_GLN_966	NZ, E_LYS_574	2HZ, E_LYS_574	2.91	1.94	13.40
COMPLEX.PDB	O, E_TYR_580	N, E_SER_575	H, E_SER_575	2.99	1.98	4.52
COMPLEX.PDB	O, E_ASP_577	OG, E_SER_575	HG, E_SER_575	2.69	1.82	21.25
COMPLEX.PDB	O, E_ASP_577	N, E_ARG_579	H, E_ARG_579	2.89	2.01	24.07
COMPLEX.PDB	OD2, E_ASP_577	NE, E_ARG_579	HE, E_ARG_579	2.81	1.80	5.72
COMPLEX.PDB	O, E_ALA_765	NH1, E_ARG_579	2HH1, E_ARG_579	2.96	1.98	12.37
COMPLEX.PDB	OD2, E_ASP_842	OH, E_TYR_580	HH, E_TYR_580	2.73	1.77	8.61
COMPLEX.PDB	O, E_VAL_573	N, E_ASP_582	H, E_ASP_582	2.90	1.90	9.87
COMPLEX.PDB	O, E_PHE_971	NZ, E_LYS_583	1HZ, E_LYS_583	2.94	2.08	26.42
COMPLEX.PDB	O, E_THR_571	N, E_GLY_584	H, E_GLY_584	2.96	2.11	27.67
COMPLEX.PDB	OD1, E_ASP_757	NH1, E_ARG_586	2HH1, E_ARG_586	2.99	2.09	22.44
COMPLEX.PDB	O, E_ASN_585	NH2, E_ARG_586	1HH2, E_ARG_586	3.00	2.00	6.66
COMPLEX.PDB	OD1, E_ASP_757	NH2, E_ARG_586	2HH2, E_ARG_586	2.88	1.93	16.41
COMPLEX.PDB	O, E_LEU_604	N, E_THR_587	H, E_THR_587	2.82	1.81	4.23
COMPLEX.PDB	OG1, E_THR_568	OG1, E_THR_587	HG1, E_THR_587	2.95	1.99	3.79
COMPLEX.PDB	O, E_LYS_567	N, E_TYR_588	H, E_TYR_588	2.77	1.76	5.35
COMPLEX.PDB	O, E_LEU_602	N, E_THR_589	H, E_THR_589	2.95	2.01	18.23
COMPLEX.PDB	O, E_GLY_565	N, E_TRP_590	H, E_TRP_590	2.98	1.98	8.82
COMPLEX.PDB	O, E_LEU_600	N, E_THR_591	H, E_THR_591	2.97	1.98	12.11
COMPLEX.PDB	OG, E_SER_564	OG1, E_THR_591	HG1, E_THR_591	2.79	1.86	13.03
COMPLEX.PDB	O, E_TYR_598	N, E_VAL_593	H, E_VAL_593	2.91	1.90	6.90

COMPLEX.PDB	OE1, E_GLU_87	N, E_GLY_595	H, E_GLY_595	2.98	2.15	28.93
COMPLEX.PDB	O, E_VAL_593	N, E_THR_596	H, E_THR_596	2.94	1.98	15.05
COMPLEX.PDB	O, E_MET_559	OG, E_SER_599	HG, E_SER_599	2.70	1.74	9.61
COMPLEX.PDB	O, E_THR_591	N, E_LEU_600	H, E_LEU_600	2.94	1.92	0.64
COMPLEX.PDB	O, E_PHE_513	N, E_ALA_601	H, E_ALA_601	2.83	1.84	11.64
COMPLEX.PDB	O, E_THR_589	N, E_LEU_602	H, E_LEU_602	2.91	1.93	12.09
COMPLEX.PDB	O, E_TYR_511	N, E_VAL_603	H, E_VAL_603	2.84	1.86	12.70
COMPLEX.PDB	O, E_THR_587	N, E_LEU_604	H, E_LEU_604	2.90	1.90	8.12
COMPLEX.PDB	O, E_PRO_605	N, E_TYR_607	H, E_TYR_607	2.80	1.96	27.81
COMPLEX.PDB	O, E_PRO_605	OG, E_SER_608	HG, E_SER_608	2.78	1.81	5.72
COMPLEX.PDB	O, E_GLU_71	N, E_TYR_611	H, E_TYR_611	2.91	1.95	15.64
COMPLEX.PDB	OE1, E_GLU_71	OH, E_TYR_611	HH, E_TYR_611	2.82	1.92	18.25
COMPLEX.PDB	O, E_THR_69	N, E_LYS_613	H, E_LYS_613	2.91	1.90	6.61
COMPLEX.PDB	O, E_LEU_67	N, E_LYS_615	H, E_LYS_615	2.87	1.88	10.70
COMPLEX.PDB	OD1, E_ASP_66	NZ, E_LYS_615	1HZ, E_LYS_615	2.90	1.91	9.67
COMPLEX.PDB	O, E_ILE_616	NE2, E_GLN_622	2HE2, E_GLN_622	2.94	2.13	29.95
COMPLEX.PDB	O, E_ILE_620	N, E_ALA_623	H, E_ALA_623	2.98	2.11	25.11
COMPLEX.PDB	OE1, E_GLU_618	NZ, E_LYS_626	2HZ, E_LYS_626	2.87	1.92	16.82
COMPLEX.PDB	OE2, E_GLU_634	NZ, E_LYS_627	2HZ, E_LYS_627	2.91	2.07	28.11
COMPLEX.PDB	O, E_ARG_624	N, E_GLY_628	H, E_GLY_628	2.88	1.93	17.22
COMPLEX.PDB	OE2, E_GLU_643	NZ, E_LYS_631	2HZ, E_LYS_631	2.89	1.90	10.46
COMPLEX.PDB	O, E_LYS_631	OG, E_SER_633	HG, E_SER_633	2.88	1.92	2.30
COMPLEX.PDB	O, E_LYS_637	N, E_ASN_640	H, E_ASN_640	2.89	2.02	25.19
COMPLEX.PDB	O, E_GLU_634	ND2, E_ASN_640	2HD2, E_ASN_640	2.93	1.93	7.96
COMPLEX.PDB	O, E_ASN_640	OG, E_SER_644	HG, E_SER_644	2.63	1.71	15.39
COMPLEX.PDB	O, E_VAL_731	N, E_TYR_646	H, E_TYR_646	2.80	1.84	16.24
COMPLEX.PDB	OE2, E_GLU_738	OH, E_TYR_646	HH, E_TYR_646	2.79	1.86	12.86
COMPLEX.PDB	O, E_THR_729	N, E_PHE_648	H, E_PHE_648	2.82	1.83	9.93
COMPLEX.PDB	O, E_GLY_727	N, E_ALA_650	H, E_ALA_650	2.82	1.90	20.77
COMPLEX.PDB	O, E_ALA_650	N, E_ARG_652	H, E_ARG_652	2.82	1.94	24.68
COMPLEX.PDB	O, E_GLY_726	NH2, E_ARG_652	1HH2, E_ARG_652	2.90	2.06	28.37
COMPLEX.PDB	O, E_ALA_650	OH, E_TYR_654	HH, E_TYR_654	2.85	1.94	15.02
COMPLEX.PDB	O, E_ASN_656	NZ, E_LYS_659	3HZ, E_LYS_659	2.98	2.10	24.48
COMPLEX.PDB	O, E_ASN_663	OG, E_SER_661	HG, E_SER_661	2.78	1.93	22.64
COMPLEX.PDB	O, E_SER_661	N, E_ASN_663	H, E_ASN_663	2.83	1.93	22.11
COMPLEX.PDB	O, E_ILE_649	ND2, E_ASN_664	1HD2, E_ASN_664	2.77	1.79	10.69
COMPLEX.PDB	O, E_ASN_664	N, E_LEU_668	H, E_LEU_668	2.89	1.89	9.15
COMPLEX.PDB	O, E_PHE_667	N, E_PHE_671	H, E_PHE_671	2.81	1.84	13.45
COMPLEX.PDB	O, E_LEU_668	N, E_ASN_672	H, E_ASN_672	2.92	1.93	11.42
COMPLEX.PDB	O, E_LEU_636	ND2, E_ASN_672	1HD2, E_ASN_672	2.99	2.10	23.07
COMPLEX.PDB	O, E_ASN_670	N, E_PHE_674	H, E_PHE_674	2.92	2.01	21.21
COMPLEX.PDB	O, E_GLU_673	N, E_ARG_677	H, E_ARG_677	2.89	1.94	16.66
COMPLEX.PDB	O, E_PHE_674	N, E_LYS_678	H, E_LYS_678	2.93	2.08	27.19
COMPLEX.PDB	OD1, E_ASN_686	N, E_ASP_688	H, E_ASP_688	2.92	2.01	21.18
COMPLEX.PDB	O, E_THR_687	N, E_ASN_691	H, E_ASN_691	2.90	1.91	10.83
COMPLEX.PDB	O, E_ILE_616	ND2, E_ASN_691	1HD2, E_ASN_691	2.98	2.00	11.63
COMPLEX.PDB	O, E_ASP_688	N, E_ARG_692	H, E_ARG_692	2.94	1.94	10.04
COMPLEX.PDB	O, E_ILE_690	N, E_LEU_694	H, E_LEU_694	2.89	1.91	12.69
COMPLEX.PDB	O, E_ARG_692	N, E_ASP_696	H, E_ASP_696	2.90	1.98	19.91
COMPLEX.PDB	O, E_ILE_693	N, E_ALA_697	H, E_ALA_697	2.95	2.03	20.56
COMPLEX.PDB	O, E_ASP_696	N, E_THR_700	H, E_THR_700	2.93	1.92	4.56
COMPLEX.PDB	O, E_ASP_696	OG1, E_THR_700	HG1, E_THR_700	2.89	1.95	12.41
COMPLEX.PDB	O, E_ASN_701	N, E_GLN_705	H, E_GLN_705	2.84	1.83	2.43
COMPLEX.PDB	O, E_GLU_702	N, E_ASN_706	H, E_ASN_706	2.83	1.85	12.85
COMPLEX.PDB	O, E_THR_50	OH, E_TYR_707	HH, E_TYR_707	2.71	1.74	3.53
COMPLEX.PDB	O, E_VAL_704	N, E_SER_709	H, E_SER_709	2.91	1.93	12.67
COMPLEX.PDB	O, E_LYS_803	N, E_LYS_718	H, E_LYS_718	2.79	1.85	17.86
COMPLEX.PDB	O, E_GLN_711	NH1, E_ARG_720	2HH1, E_ARG_720	2.84	1.99	27.14

COMPLEX.PDB	O, E_GLN_711	NH2, E_ARG_720	2HH2, E_ARG_720	2.91	2.08	28.08
COMPLEX.PDB	O, E_GLY_801	N, E_PHE_721	H, E_PHE_721	2.95	1.99	14.99
COMPLEX.PDB	O, E_ARG_730	N, E_VAL_722	H, E_VAL_722	2.96	2.00	14.73
COMPLEX.PDB	O, E_VAL_799	N, E_VAL_723	H, E_VAL_723	2.85	1.84	3.87
COMPLEX.PDB	O, E_ILE_728	N, E_THR_724	H, E_THR_724	2.98	2.06	20.81
COMPLEX.PDB	OD1, E_ASP_696	OG1, E_THR_724	HG1, E_THR_724	2.95	2.05	18.78
COMPLEX.PDB	O, E_THR_724	N, E_GLY_727	H, E_GLY_727	2.99	2.09	21.97
COMPLEX.PDB	O, E_PHE_648	N, E_THR_729	H, E_THR_729	2.98	1.96	0.91
COMPLEX.PDB	O, E_VAL_722	N, E_ARG_730	H, E_ARG_730	2.92	1.93	10.71
COMPLEX.PDB	O, E_SER_644	NE, E_ARG_730	HE, E_ARG_730	2.81	1.84	13.10
COMPLEX.PDB	O, E_THR_635	NH1, E_ARG_730	2HH1, E_ARG_730	2.89	1.94	16.49
COMPLEX.PDB	O, E_ARG_720	N, E_TYR_732	H, E_TYR_732	2.89	1.87	3.44
COMPLEX.PDB	OD1, E_ASN_743	N, E_GLU_745	H, E_GLU_745	2.94	1.94	8.91
COMPLEX.PDB	OD1, E_ASP_725	OH, E_TYR_747	HH, E_TYR_747	2.67	1.74	12.91
COMPLEX.PDB	O, E_GLU_745	N, E_GLU_748	H, E_GLU_748	2.92	1.93	11.37
COMPLEX.PDB	OD2, E_ASP_582	NE, E_ARG_754	HE, E_ARG_754	2.90	1.89	4.50
COMPLEX.PDB	OD1, E_ASP_843	NH1, E_ARG_754	2HH1, E_ARG_754	2.92	2.03	23.47
COMPLEX.PDB	OD1, E_ASP_582	NH2, E_ARG_754	1HH2, E_ARG_754	2.83	1.94	23.45
COMPLEX.PDB	OD2, E_ASP_843	NH2, E_ARG_754	2HH2, E_ARG_754	2.89	1.95	18.36
COMPLEX.PDB	O, E_PHE_751	N, E_SER_755	H, E_SER_755	2.94	1.99	16.83
COMPLEX.PDB	O, E_PHE_751	OG, E_SER_755	HG, E_SER_755	2.72	1.75	6.55
COMPLEX.PDB	O, E_LYS_753	N, E_ASP_757	H, E_ASP_757	2.99	2.03	15.55
COMPLEX.PDB	OD1, E_ASP_582	ND2, E_ASN_758	1HD2, E_ASN_758	2.94	1.96	11.82
COMPLEX.PDB	O, E_ARG_754	ND2, E_ASN_758	2HD2, E_ASN_758	2.92	1.97	16.08
COMPLEX.PDB	O, E_SER_783	N, E_VAL_762	H, E_VAL_762	2.88	1.88	6.26
COMPLEX.PDB	O, E_MET_781	N, E_THR_764	H, E_THR_764	2.81	1.83	13.11
COMPLEX.PDB	OH, E_TYR_580	N, E_ALA_765	H, E_ALA_765	2.97	1.98	9.62
COMPLEX.PDB	OE2, E_GLU_777	N, E_ALA_775	H, E_ALA_775	2.80	1.83	14.49
COMPLEX.PDB	O, E_ALA_775	N, E_GLY_779	H, E_GLY_779	2.87	1.93	18.01
COMPLEX.PDB	O, E_ILE_802	N, E_VAL_782	H, E_VAL_782	2.84	1.85	11.63
COMPLEX.PDB	O, E_VAL_762	N, E_SER_783	H, E_SER_783	2.85	1.86	11.00
COMPLEX.PDB	OG, E_SER_755	OG, E_SER_783	HG, E_SER_783	2.82	1.99	26.18
COMPLEX.PDB	O, E_VAL_800	N, E_LYS_784	H, E_LYS_784	2.90	1.91	10.94
COMPLEX.PDB	O, E_ALA_798	N, E_VAL_786	H, E_VAL_786	2.85	1.83	3.10
COMPLEX.PDB	OE2, E_GLU_787	OH, E_TYR_789	HH, E_TYR_789	2.88	2.00	19.65
COMPLEX.PDB	O, E_LEU_788	N, E_LEU_795	H, E_LEU_795	2.92	1.92	8.04
COMPLEX.PDB	O, E_VAL_723	N, E_VAL_799	H, E_VAL_799	2.85	1.85	7.03
COMPLEX.PDB	O, E_LYS_784	N, E_VAL_800	H, E_VAL_800	2.96	1.96	9.55
COMPLEX.PDB	O, E_PHE_721	N, E_GLY_801	H, E_GLY_801	2.95	2.01	17.74
COMPLEX.PDB	O, E_VAL_782	N, E_ILE_802	H, E_ILE_802	2.91	1.92	11.23
COMPLEX.PDB	O, E_ALA_719	N, E_LYS_803	H, E_LYS_803	2.83	1.85	11.86
COMPLEX.PDB	OG, E_SER_778	NZ, E_LYS_803	3HZ, E_LYS_803	2.98	2.03	15.64
COMPLEX.PDB	O, E_ILE_780	N, E_ILE_804	H, E_ILE_804	2.79	1.78	4.97
COMPLEX.PDB	O, E_GLY_716	N, E_ASP_805	H, E_ASP_805	2.90	1.89	1.39
COMPLEX.PDB	OD2, E_ASP_805	OG, E_SER_808	HG, E_SER_808	2.69	1.73	8.01
COMPLEX.PDB	O, E_SER_808	N, E_ASN_812	H, E_ASN_812	2.99	2.02	14.40
COMPLEX.PDB	O, E_TRP_809	N, E_PHE_813	H, E_PHE_813	2.83	1.95	23.97
COMPLEX.PDB	O, E_ILE_810	N, E_THR_814	H, E_THR_814	2.89	1.93	14.55
COMPLEX.PDB	O, E_ILE_810	OG1, E_THR_814	HG1, E_THR_814	2.70	1.74	5.57
COMPLEX.PDB	O, E_GLU_811	N, E_LYS_815	H, E_LYS_815	2.91	1.95	15.65
COMPLEX.PDB	OD1, E_ASP_853	NE, E_ARG_831	HE, E_ARG_831	2.89	2.00	23.79
COMPLEX.PDB	O, E_ASN_851	N, E_ASN_832	H, E_ASN_832	2.95	1.94	4.98
COMPLEX.PDB	O, E_ASP_842	N, E_GLY_845	H, E_GLY_845	2.91	1.98	19.51
COMPLEX.PDB	OD1, E_ASP_842	N, E_PHE_846	H, E_PHE_846	2.82	1.84	13.47
COMPLEX.PDB	O, E_ILE_840	N, E_LEU_848	H, E_LEU_848	2.94	1.95	9.65
COMPLEX.PDB	O, E_LYS_830	ND2, E_ASN_851	1HD2, E_ASN_851	2.83	1.94	23.05
COMPLEX.PDB	OD1, E_ASP_837	ND2, E_ASN_851	2HD2, E_ASN_851	2.91	1.91	8.10
COMPLEX.PDB	OD1, E_ASP_837	ND1, E_HIS_852	HD1, E_HIS_852	2.87	1.91	17.61

COMPLEX.PDB	O, E_HIS_852	N, E_ASP_854	H, E_ASP_854	2.79	1.89	22.92
COMPLEX.PDB	O, E_LEU_847	N, E_GLY_860	H, E_GLY_860	2.82	1.85	13.93
COMPLEX.PDB	OE1, E_GLU_865	NE, E_ARG_861	HE, E_ARG_861	2.98	2.01	12.72
COMPLEX.PDB	O, E_GLY_845	N, E_PHE_863	H, E_PHE_863	2.84	1.82	3.36
COMPLEX.PDB	O, E_PHE_862	N, E_GLU_865	H, E_GLU_865	2.93	1.96	13.91
COMPLEX.PDB	O, E_PHE_863	N, E_ASP_867	H, E_ASP_867	2.82	1.81	5.29
COMPLEX.PDB	O, E_PRO_868	N, E_ARG_872	H, E_ARG_872	2.98	2.02	16.64
COMPLEX.PDB	O, E_MET_870	N, E_LEU_874	H, E_LEU_874	2.89	1.94	17.19
COMPLEX.PDB	O, E_ARG_872	N, E_ASN_876	H, E_ASN_876	2.98	2.02	15.46
COMPLEX.PDB	O, E_HIS_873	N, E_ILE_877	H, E_ILE_877	2.94	1.98	14.98
COMPLEX.PDB	O, E_ILE_877	OG, E_SER_878	HG, E_SER_878	2.62	1.70	14.57
COMPLEX.PDB	O, E_PHE_970	N, E_ALA_881	H, E_ALA_881	2.97	2.11	26.30
COMPLEX.PDB	O, E_GLN_966	N, E_SER_885	H, E_SER_885	2.93	1.97	16.36
COMPLEX.PDB	O, E_THR_964	N, E_ASP_887	H, E_ASP_887	2.84	1.84	8.65
COMPLEX.PDB	O, E_GLN_528	NE2, E_GLN_889	1HE2, E_GLN_889	2.88	1.93	16.41
COMPLEX.PDB	OG1, E_THR_964	OG, E_SER_890	HG, E_SER_890	2.71	1.79	15.36
COMPLEX.PDB	O, E_GLN_900	N, E_ALA_902	H, E_ALA_902	2.97	2.08	23.31
COMPLEX.PDB	O, E_GLY_895	NH2, E_ARG_905	1HH2, E_ARG_905	2.95	1.99	14.37
COMPLEX.PDB	O, E_TRP_921	N, E_THR_923	H, E_THR_923	2.92	2.05	25.12
COMPLEX.PDB	O, E_LEU_933	N, E_SER_936	H, E_SER_936	2.83	1.85	11.53
COMPLEX.PDB	O, E_LEU_933	OG, E_SER_936	HG, E_SER_936	2.78	1.82	7.52
COMPLEX.PDB	O, E_THR_954	OG, E_SER_956	HG, E_SER_956	2.91	1.98	13.24
COMPLEX.PDB	OG, E_SER_906	OG, E_SER_958	HG, E_SER_958	2.98	2.16	27.41
COMPLEX.PDB	O, E_SER_890	N, E_CYS_962	H, E_CYS_962	2.88	1.90	12.44
COMPLEX.PDB	O, E_ASP_887	N, E_THR_964	H, E_THR_964	2.98	1.99	9.13
COMPLEX.PDB	O, E_SER_885	N, E_GLN_966	H, E_GLN_966	2.79	1.78	6.01
COMPLEX.PDB	O, E_ALA_881	N, E_PHE_970	H, E_PHE_970	2.91	1.94	13.36
COMPLEX.PDB	OD1, E_ASN_973	OG1, E_THR_975	HG1, E_THR_975	2.75	1.83	15.01
COMPLEX.PDB	OE1, E_GLU_994	OG, E_SER_977	HG, E_SER_977	2.61	1.64	6.33
COMPLEX.PDB	O, E_VAL_993	N, E_PHE_978	H, E_PHE_978	2.94	1.93	7.59
COMPLEX.PDB	O, E_ARG_989	N, E_LEU_982	H, E_LEU_982	2.96	2.03	19.41
COMPLEX.PDB	OD1, E_ASP_983	OG, E_SER_988	HG, E_SER_988	2.63	1.65	5.60
COMPLEX.PDB	O, E_LEU_982	N, E_ARG_989	H, E_ARG_989	2.93	2.01	20.71
COMPLEX.PDB	OD2, E_ASP_867	NH2, E_ARG_989	2HH2, E_ARG_989	2.90	1.90	8.63
COMPLEX.PDB	O, E_GLY_980	N, E_PHE_991	H, E_PHE_991	2.93	1.92	5.82
COMPLEX.PDB	O, E_PHE_978	N, E_VAL_993	H, E_VAL_993	2.79	1.80	9.59
COMPLEX.PDB	O, E_LYS_976	N, E_LYS_995	H, E_LYS_995	2.85	1.89	14.44
COMPLEX.PDB	O, E_TYR_761	OG1, E_THR_999	HG1, E_THR_999	2.88	1.95	13.29

Table 3: The side chain and main chain hydrogen bonding networks within the structural model represented in COMPLEX.pdb. In this table, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).

PDB	Acceptor (A)	Donor (D)	Hydrogen (H)	D-A (Å)	H-A (Å)	$\angle ADH$(°)
COMPLEX.PDB	OG, E_SER_29	OG1, E_THR_32	HG1, E_THR_32	2.72	1.76	6.24
COMPLEX.PDB	OE1, E_GLU_702	OH, E_TYR_64	HH, E_TYR_64	2.63	1.66	4.27
COMPLEX.PDB	OE2, E_GLU_103	NZ, E_LYS_106	1HZ, E_LYS_106	2.94	1.96	12.59
COMPLEX.PDB	OD1, E_ASN_184	NE2, E_HIS_111	HE2, E_HIS_111	2.88	1.88	10.04
COMPLEX.PDB	OE2, E_GLU_115	NE1, E_TRP_113	HE1, E_TRP_113	2.99	2.09	21.85
COMPLEX.PDB	OD2, E_ASP_116	OG, E_SER_119	HG, E_SER_119	2.66	1.71	9.60
COMPLEX.PDB	OD1, E_ASP_234	NZ, E_LYS_128	3HZ, E_LYS_128	2.94	1.95	10.09
COMPLEX.PDB	OD2, E_ASP_129	NE, E_ARG_144	HE, E_ARG_144	2.79	1.81	12.37
COMPLEX.PDB	OD2, E_ASP_234	NE2, E_HIS_167	HE2, E_HIS_167	2.83	1.86	15.02
COMPLEX.PDB	OE2, E_GLU_182	NE1, E_TRP_185	HE1, E_TRP_185	2.92	1.92	8.41
COMPLEX.PDB	OE1, E_GLN_206	ND2, E_ASN_196	2HD2, E_ASN_196	2.92	1.94	11.76
COMPLEX.PDB	OD1, E_ASP_200	OG1, E_THR_202	HG1, E_THR_202	2.72	1.76	6.38
COMPLEX.PDB	OE1, E_GLU_182	OG, E_SER_210	HG, E_SER_210	2.66	1.69	4.87
COMPLEX.PDB	OD1, E_ASP_190	NE, E_ARG_216	HE, E_ARG_216	2.91	2.02	23.66
COMPLEX.PDB	OD2, E_ASP_190	NH2, E_ARG_216	1HH2, E_ARG_216	3.00	2.07	19.79
COMPLEX.PDB	OD1, E_ASP_130	OG1, E_THR_229	HG1, E_THR_229	2.76	1.81	9.95
COMPLEX.PDB	OD2, E_ASP_225	NZ, E_LYS_232	2HZ, E_LYS_232	2.92	1.96	15.31
COMPLEX.PDB	OE1, E_GLU_278	NH1, E_ARG_240	2HH1, E_ARG_240	2.96	2.06	22.46
COMPLEX.PDB	OE1, E_GLU_278	NH2, E_ARG_240	2HH2, E_ARG_240	2.88	1.94	17.95
COMPLEX.PDB	OE1, E_GLN_445	NE2, E_GLN_246	2HE2, E_GLN_246	2.93	1.98	15.85
COMPLEX.PDB	OD1, E_ASP_287	NZ, E_LYS_252	3HZ, E_LYS_252	2.98	1.98	8.55
COMPLEX.PDB	OD1, E_ASP_259	OG, E_SER_261	HG, E_SER_261	2.70	1.76	11.26
COMPLEX.PDB	OD2, E_ASP_363	OG, E_SER_263	HG, E_SER_263	2.97	2.07	18.12
COMPLEX.PDB	OE1, E_GLN_424	OG1, E_THR_282	HG1, E_THR_282	2.98	2.03	7.37
COMPLEX.PDB	OD2, E_ASP_287	OG, E_SER_284	HG, E_SER_284	2.69	1.72	5.06
COMPLEX.PDB	OE2, E_GLU_281	NZ, E_LYS_319	1HZ, E_LYS_319	2.86	2.03	29.01
COMPLEX.PDB	OE1, E_GLU_371	NZ, E_LYS_334	3HZ, E_LYS_334	2.94	1.96	13.07
COMPLEX.PDB	OD2, E_ASP_253	NH2, E_ARG_351	1HH2, E_ARG_351	2.98	2.07	20.97
COMPLEX.PDB	OH, E_TYR_347	NZ, E_LYS_356	1HZ, E_LYS_356	2.92	1.95	13.13
COMPLEX.PDB	OH, E_TYR_333	OG1, E_THR_362	HG1, E_THR_362	2.73	1.83	17.19
COMPLEX.PDB	OE2, E_GLU_412	NH1, E_ARG_396	1HH1, E_ARG_396	2.89	1.91	11.57
COMPLEX.PDB	OE2, E_GLU_412	OH, E_TYR_410	HH, E_TYR_410	2.72	1.77	11.16
COMPLEX.PDB	OG1, E_THR_461	OH, E_TYR_450	HH, E_TYR_450	2.76	1.91	23.68
COMPLEX.PDB	OD1, E_ASP_491	OG1, E_THR_461	HG1, E_THR_461	2.75	1.78	5.29
COMPLEX.PDB	OD1, E_ASN_475	ND2, E_ASN_478	1HD2, E_ASN_478	2.92	1.93	8.35
COMPLEX.PDB	OD2, E_ASP_496	OG, E_SER_493	HG, E_SER_493	2.79	1.85	10.99
COMPLEX.PDB	OE2, E_GLU_748	NH2, E_ARG_503	2HH2, E_ARG_503	2.87	1.91	15.22
COMPLEX.PDB	OH, E_TYR_607	ND2, E_ASN_509	2HD2, E_ASN_509	2.97	2.01	14.80
COMPLEX.PDB	OE2, E_GLU_546	OH, E_TYR_511	HH, E_TYR_511	2.64	1.68	7.93
COMPLEX.PDB	OD1, E_ASP_286	ND2, E_ASN_518	1HD2, E_ASN_518	2.98	2.02	15.09
COMPLEX.PDB	OD1, E_ASP_285	OH, E_TYR_520	HH, E_TYR_520	2.61	1.65	7.75
COMPLEX.PDB	OE2, E_GLU_546	NE2, E_HIS_524	HE2, E_HIS_524	2.89	1.87	3.11
COMPLEX.PDB	OE1, E_GLU_546	NZ, E_LYS_552	1HZ, E_LYS_552	2.88	1.92	14.82
COMPLEX.PDB	OD2, E_ASP_541	NE, E_ARG_556	HE, E_ARG_556	2.92	1.95	14.11
COMPLEX.PDB	OD1, E_ASN_557	NH1, E_ARG_556	1HH1, E_ARG_556	2.90	2.00	22.19
COMPLEX.PDB	OD1, E_ASP_541	NH2, E_ARG_556	1HH2, E_ARG_556	2.85	1.84	6.22
COMPLEX.PDB	OE1, E_GLU_554	NZ, E_LYS_567	1HZ, E_LYS_567	2.96	2.06	21.68
COMPLEX.PDB	OE1, E_GLN_966	NZ, E_LYS_574	2HZ, E_LYS_574	2.91	1.94	13.40
COMPLEX.PDB	OD2, E_ASP_577	NE, E_ARG_579	HE, E_ARG_579	2.81	1.80	5.72
COMPLEX.PDB	OD2, E_ASP_842	OH, E_TYR_580	HH, E_TYR_580	2.73	1.77	8.61
COMPLEX.PDB	OD1, E_ASP_757	NH1, E_ARG_586	2HH1, E_ARG_586	2.99	2.09	22.44
COMPLEX.PDB	OD1, E_ASP_757	NH2, E_ARG_586	2HH2, E_ARG_586	2.88	1.93	16.41
COMPLEX.PDB	OG1, E_THR_568	OG1, E_THR_587	HG1, E_THR_587	2.95	1.99	3.79
COMPLEX.PDB	OG, E_SER_564	OG1, E_THR_591	HG1, E_THR_591	2.79	1.86	13.03
COMPLEX.PDB	OE1, E_GLU_71	OH, E_TYR_611	HH, E_TYR_611	2.82	1.92	18.25
COMPLEX.PDB	OD1, E_ASP_66	NZ, E_LYS_615	1HZ, E_LYS_615	2.90	1.91	9.67
COMPLEX.PDB	OE1, E_GLU_618	NZ, E_LYS_626	2HZ, E_LYS_626	2.87	1.92	16.82

COMPLEX.PDB	OE2, E_GLU_634	NZ, E_LYS_627	2HZ, E_LYS_627	2.91	2.07	28.11
COMPLEX.PDB	OE2, E_GLU_643	NZ, E_LYS_631	2HZ, E_LYS_631	2.89	1.90	10.46
COMPLEX.PDB	OE2, E_GLU_738	OH, E_TYR_646	HH, E_TYR_646	2.79	1.86	12.86
COMPLEX.PDB	OD1, E_ASP_696	OG1, E_THR_724	HG1, E_THR_724	2.95	2.05	18.78
COMPLEX.PDB	OD1, E_ASP_725	OH, E_TYR_747	HH, E_TYR_747	2.67	1.74	12.91
COMPLEX.PDB	OD2, E_ASP_582	NE, E_ARG_754	HE, E_ARG_754	2.90	1.89	4.50
COMPLEX.PDB	OD1, E_ASP_843	NH1, E_ARG_754	2HH1, E_ARG_754	2.92	2.03	23.47
COMPLEX.PDB	OD1, E_ASP_582	NH2, E_ARG_754	1HH2, E_ARG_754	2.83	1.94	23.45
COMPLEX.PDB	OD2, E_ASP_843	NH2, E_ARG_754	2HH2, E_ARG_754	2.89	1.95	18.36
COMPLEX.PDB	OD1, E_ASP_582	ND2, E_ASN_758	1HD2, E_ASN_758	2.94	1.96	11.82
COMPLEX.PDB	OG, E_SER_755	OG, E_SER_783	HG, E_SER_783	2.82	1.99	26.18
COMPLEX.PDB	OE2, E_GLU_787	OH, E_TYR_789	HH, E_TYR_789	2.88	2.00	19.65
COMPLEX.PDB	OG, E_SER_778	NZ, E_LYS_803	3HZ, E_LYS_803	2.98	2.03	15.64
COMPLEX.PDB	OD2, E_ASP_805	OG, E_SER_808	HG, E_SER_808	2.69	1.73	8.01
COMPLEX.PDB	OD1, E_ASP_853	NE, E_ARG_831	HE, E_ARG_831	2.89	2.00	23.79
COMPLEX.PDB	OD1, E_ASP_837	ND2, E_ASN_851	2HD2, E_ASN_851	2.91	1.91	8.10
COMPLEX.PDB	OD1, E_ASP_837	ND1, E_HIS_852	HD1, E_HIS_852	2.87	1.91	17.61
COMPLEX.PDB	OE1, E_GLU_865	NE, E_ARG_861	HE, E_ARG_861	2.98	2.01	12.72
COMPLEX.PDB	OG1, E_THR_964	OG, E_SER_890	HG, E_SER_890	2.71	1.79	15.36
COMPLEX.PDB	OG, E_SER_906	OG, E_SER_958	HG, E_SER_958	2.98	2.16	27.41
COMPLEX.PDB	OD1, E_ASN_973	OG1, E_THR_975	HG1, E_THR_975	2.75	1.83	15.01
COMPLEX.PDB	OE1, E_GLU_994	OG, E_SER_977	HG, E_SER_977	2.61	1.64	6.33
COMPLEX.PDB	OD1, E_ASP_983	OG, E_SER_988	HG, E_SER_988	2.63	1.65	5.60
COMPLEX.PDB	OD2, E_ASP_867	NH2, E_ARG_989	2HH2, E_ARG_989	2.90	1.90	8.63

Table 4: The side chain hydrogen bonding networks within the structural model represented in COMPLEX.pdb. In this table, the residue naming scheme is **Chain ID_residue name_residue number**, $\angle ADH$ represents the angle formed by acceptor (A), donor (D) and hydrogen (H) ($\angle ADH$).